

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 17, 2003, 07:20:40 ; Search time 13.4351 Seconds  
(without alignments)  
228.975 Million cell updates/sec

Title: US-09-787-082-5  
Perfect score: 190  
Sequence: 1 CKGKGAKCSRLMYDCTGSCRSRKGKTRNGLPG 32  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151	79.5	25	2 JH0700	omega-conotoxin MV
2	120	63.2	25	2 JH0701	omega-conotoxin MV
3	112.5	59.2	29	2 JH0699	omega-conotoxin MV
4	104	54.7	29	2 A58537	omega-conotoxin MV
5	97.5	51.3	26	2 C44379	omega-conotoxin GV
6	75.5	39.7	29	2 A43620	omega-conotoxin GV
7	75.5	39.7	29	2 B43620	omega-conotoxin GV
8	70	36.8	686	2 T25987	hypothetical prote
9	64	33.7	72	2 S39417	metallothionein 10
10	61.5	32.4	610	2 JC7530	vascular apoptosis
11	60.5	31.8	66	2 S58086	metallothionein 3
12	60.5	31.8	68	2 A46034	metallothionein 3
13	60.5	31.8	68	2 F87866	growth inhibitor
14	59.5	31.3	751	2 F87789	protein C34G6.2 i
15	59	31.1	72	2 S39416	metallothionein 10
16	58	30.5	27	2 S19619	delta-conotoxin Tx
17	58	30.5	78	2 S12513	delta-conotoxin Tx
18	57.5	30.3	78	1 T12B1A	proteinase inhibit
19	57.5	30.3	78	1 T12B1B	proteinase inhibit
20	57.5	30.3	1369	2 S70713	protein-tyrosine k
21	57	30.0	24	2 B44379	omega-conotoxin SV
22	57	30.0	72	2 S39419	metallothionein 10
23	56.5	29.7	73	1 NTKN6G	omega-conotoxin GV
24	56	29.5	318	2 T05569	hypothetical prote
25	56	29.5	1051	2 JC4091	glycoprotein A - p
26	56	29.5	2664	2 T28626	variant-specific s
27	55.5	28.2	79	1 T1FB2	proteinase inhibit
28	55	28.9	60	1 SMH01A	metallothionein 1A
29	55	28.9	65	2 A38739	metallothionein -

ALIGNMENTS

RESULT 1

JH0700

omega-conotoxin MWIIA [validated] - cone shell (Conus magus)

C:Species: Conus magus (magus cone)

C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 15-Sep-2000

C:Accession: JH0700; C60133; A34115

R:Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.  
Neuron 9, 69-77, 1992

A:Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.

A:Reference number: JH0699; MUID:92337922; PMID:1352986

A:Accession: JH0700

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-25 <HIL>

R:Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Sa

Science 230, 1338-1343, 1985

A:Title: Peptide neurotoxins from fish-hunting cone snails.

A:Reference number: A43620; MUID:86070213; PMID:4071055

A:Accession: C60133

A:Molecule type: protein

A:Residues: 1-25 <OLI>

R:Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R

Biochemistry 26, 2086-2090, 1987

A:Title: Neuronal calcium channel antagonists. Discrimination between calcium channel

A:Reference number: A34115; MUID:87299637; PMID:2441741

A:Contents: annotation

R:Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.

submitted to the Brookhaven Protein Data Bank, August 1996

A:Reference number: A67648; PDB:1MVI

A:Contents: annotation; conformation by (1)H-NMR, residues 1-25

R:Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.

J. Mol. Biol. 263, 297-310, 1996

A:Title: A consensus structure for omega-conotoxins with different selectivities for

A:Reference number: A58619; MUID:97070382; PMID:8913308

A:Contents: annotation; conformation by (1)H-NMR

R:Kohn, T.; Kim, J.I.; Kobayashi, K.; Koder, Y.; Maeda, T.; Sato, K.

submitted to the Brookhaven Protein Data Bank, April 1995

A:Reference number: A66296; PDB:1OMG

A:Contents: annotation; conformation by (1)H-NMR, residues 1-25

R:Kohn, T.; Kim, J.I.; Kobayashi, K.; Koder, Y.; Maeda, T.; Sato, K.

Biochemistry 34, 10256-10265, 1995

A:Title: Three-dimensional structure in solution of the calcium channel blocker omega

A:Reference number: A58627; MUID:95367555; PMID:7640281

A:Contents: annotation; conformation by (1)H-NMR

C:Superfamily: omega-conotoxin

C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel

F:1-16, 8-20, 15-25/Disulfide bonds: #status predicted

F:25/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 79.5%; Score 151; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 2.3e-10;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





1.  $\frac{1}{2}$

NOTES/REMARKS

A;Molecule type: protein  
 A;Residues: 1-72 <MAC>  
 C;Superfamily: metallothionein  
 C;Keywords: metal binding

Query Match 31.1%; Score 59; DB 2; Length 72;  
 Best Local Similarity 46.4%; Pred. NO. 5.8;  
 Matches 13; Conservative 1; Mismatches 12; Indels 2; Gaps 2;

QY 1 CKGKGAKCSRLMYDC-CTGSCRSRK-CT 26  
 Db 31 CSGADCKCSGCKVVKCSGRCECGGCT 58

Search completed: March 17, 2003, 07:27:25  
 Job time : 15.4351 secs

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